

Table S6: Protein disorder abundance for disorder regions > 30 residues.

Organism ^a	"%long30" ^b		
	MD ^c	IUPred ^c	NORSnet ^c
Thermophiles			
<i>Thermosynechococcus elongatus</i> BP-1	12 ± 1	5.4 ± 0.9	3.2 ± 0.6
<i>Clostridium clariflavum</i> DSM 19732	13 ± 1	4.0 ± 0.6	1.1 ± 0.3
<i>Streptococcus thermophilus</i> LMG 18311	16 ± 2	5 ± 1	2.0 ± 0.6
Hyperthermophiles			
<i>Aeropyrum pernix</i> K1	9 ± 1	2.8 ± 0.7	0.5 ± 0.4
<i>Pyrococcus horikoshii</i> OT3	9 ± 1	1.6 ± 0.5	4.0 ± 0.8
Psychrophiles			
<i>Desulfotalea psychrophila</i> LSv54	12 ± 1	3.9 ± 0.6	1.5 ± 0.4
<i>Colwellia psychrerythraea</i> 34H	12.2 ± 0.9	3.8 ± 0.5	1.1 ± 0.3
<i>Shewanella woodyi</i> ATCC 51908	11.3 ± 0.8	4.3 ± 0.5	2.0 ± 0.4
Psychrotolerants			
<i>Methanococcoides burtonii</i> DSM 6242	10 ± 1	3.9 ± 0.7	1.2 ± 0.4
<i>Leuconostoc citreum</i> KM20	14 ± 1	6 ± 1	1.4 ± 0.5
<i>Bacillus weihenstephanensis</i> KBAB4	14.0 ± 0.9	4.7 ± 0.5	1.1 ± 0.3
<i>Rhodoferax ferrireducens</i> T118	11.8 ± 0.9	6.2 ± 0.7	2.5 ± 0.4
Halophiles			
<i>Haloarcula marismortui</i> ATCC 43049	22 ± 1	27 ± 1	4.6 ± 0.6
<i>Halobacterium</i> sp. NRC-1	21 ± 1	24 ± 2	3.2 ± 0.7
<i>Marinobacter aquaeolei</i> VT8	14 ± 1	9.9 ± 0.8	3.0 ± 0.5
Alkalophile			
<i>Bacillus halodurans</i> C-125	13 ± 1	5.9 ± 0.7	1.2 ± 0.3
Radiation resistant			
<i>Deinococcus deserti</i> VCD115	11 ± 1	11.4 ± 0.9	3.3 ± 0.6
<i>Deinococcus maricopensis</i> DSM 21211	10 ± 1	11 ± 1	2.5 ± 0.5
<i>Deinococcus radiodurans</i>	14 ± 1	17 ± 1	5.2 ± 0.7
Taxonomic neighbors (mesophiles)			

<i>Caulobacter vibrioides</i>	16 ± 1	11 ± 1	4.5 ± 0.6
<i>Chromobacterium violaceum</i> ATCC 12472	12.9 ± 0.9	7.6 ± 0.7	3.0 ± 0.4
<i>Clostridium acetobutylicum</i>	13 ± 1	2.4 ± 0.4	0.6 ± 0.2
<i>Corynebacterium glutamicum</i>	16 ± 1	12 ± 1	5.4 ± 0.7
<i>Desulfovibrio vulgaris</i> str. Hildenborough	19 ± 1	14 ± 1	3.7 ± 0.6
<i>Geobacter metallireducens</i> GS-15	12 ± 1	6.3 ± 0.8	2.3 ± 0.4
<i>Geobacter sulfurreducens</i> PCA	13 ± 1	6.9 ± 0.8	2.9 ± 0.5
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	16 ± 1	5.0 ± 0.8	1.8 ± 0.5
<i>Listeria innocua</i>	15 ± 1	5.3 ± 0.7	1.2 ± 0.4
<i>Methanosarcina mazei</i> Go1	14 ± 1	7.0 ± 0.8	2.5 ± 0.5
<i>Methanococcus maripaludis</i> S2	12 ± 1	1.9 ± 0.6	0.5 ± 0.3
<i>Nitrosomonas europaea</i> ATCC 19718	14 ± 1	6.3 ± 0.9	2.3 ± 0.6
<i>Pseudoalteromonas atlantica</i> T6c	10.8 ± 0.9	5.6 ± 0.6	2.0 ± 0.4
<i>Rhodopseudomonas palustris</i> CGA009	14.9 ± 0.9	11.0 ± 0.8	4.5 ± 0.6
<i>Rhodospirillum rubrum</i> ATCC 11170	14 ± 1	10.5 ± 0.9	3.7 ± 0.5
<i>Rhodobacter sphaeroides</i> 2.4.1	14 ± 1	9.9 ± 0.9	3.1 ± 0.5
<i>Shewanella oneidensis</i>	16 ± 1	4.3 ± 0.5	1.9 ± 0.4
<i>Ruegeria pomeroyi</i> DSS-3	9.3 ± 0.8	6.3 ± 0.7	1.6 ± 0.4
<i>Streptomyces coelicolor</i>	18.9 ± 0.8	25.8 ± 0.9	8.2 ± 0.6
<i>Synechococcus elongatus</i> PCC 6301	13 ± 1	6.1 ± 0.9	4.0 ± 0.7
<i>Synechocystis</i> sp. PCC 6803 substr. Kazusa	15 ± 1	6.5 ± 0.8	3.4 ± 0.6
Eukaryotes			
<i>Arabidopsis thaliana</i>	40.9 ± 0.5	29.8 ± 0.5	31.5 ± 0.5
<i>Caenorhabditis elegans</i>	39.8 ± 0.6	32.3 ± 0.6	28.5 ± 0.5
<i>Dictyostelium discoideum</i>	46.4 ± 0.8	43.8 ± 0.8	28.3 ± 0.7
<i>Drosophila melanogaster</i>	50.7 ± 0.8	45.8 ± 0.8	39.9 ± 0.8
<i>Schizosaccharomyces pombe</i> 972h-	43 ± 1	30 ± 1	29 ± 1
<i>Saccharomyces cerevisiae</i> S288c	46 ± 1	35 ± 1	30 ± 1

- a. Organism marks the full name of the organism where grey cells correspond to the environments; Taxonomic neighbors correspond to organisms that are related in phylogeny to the extremophiles described in this study. Eukaryotes picked at random from the set of completely sequenced organisms in UniProt.
- b. Disorder %long30 refers to the percentage of proteins in a proteome that contains at least one region with ≥ 30 consecutive residues predicted as disordered.
- c. <MD | IUPred | NORSnet> refer to the three prediction methods used, in order to catch the different “flavors” of disorder.